

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 15, 2002, 09:04:27 ; Search time 14.7051 Seconds
(Without alignment)
3334.117 Million cell updates/sec

Title: US-09-972-268-10

Perfect score: 2711

Sequence: 1 MARIPEPSLCPGSGKAQLS.....KHONNDPKRYIDREHYV 510

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0 %

Maximum Match 100 %

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1173.5	43.3	407	2 T08732	hypothetical prote
2	565.5	20.9	518	2 JC4024	poliovirus recepto
3	540	19.9	530	2 A53437	poliovirus recepto
4	527	19.4	538	2 I68093	PRR2 delta - human
5	467	17.2	467	1 HLMSP3	poliovirus recepto
6	455	16.8	478	2 I53960	PRR2 alpha - human
7	418	15.4	392	2 B44194	poliovirus recepto
8	418	15.4	417	2 A44194	poliovirus recepto
9	402	14.8	392	1 RMWRPD	poliovirus recepto
10	402	14.8	417	1 RMWRPD	poliovirus recepto
11	326.5	12.0	416	2 A54017	colon carcinoma-as
12	229.5	8.5	764	2 A49448	irregular chlam C
13	204.5	7.5	4391	2 A38096	perlecan precursor
14	196.5	7.2	5175	2 T20392	hypothetical prote
15	187.5	6.9	274	2 T43290	hemocytin precurs
16	187.5	6.9	274	2 A47639	hemocytin precurs
17	181.5	6.7	1896	2 T08851	OX-2 membrane glyco
18	178	6.6	588	2 JH0506	down syndrome cell
19	178	6.6	588	2 A45254	adhesion molecule
20	177.5	6.5	853	2 IUBONC	surface glycoprote
21	177	6.5	636	1 A61084	neural cell adhesi
22	177	6.5	637	2 B33785	myelin-associated
23	176	6.5	7962	2 I38346	myelin-associated
24	175	6.5	582	1 BNR73S	myelin-associated
25	175	6.5	626	1 BNR73S	myelin-associated
26	174	6.4	1091	2 A58532	glial cell membran
27	172.5	6.3	365	2 UC7780	heparan sulfate pr
28	170.5	6.3	365	2 UC7780	heparan sulfate pr
29	164.5	6.1	847	2 JH0371	B-cell adhesion pr

30	162.5	6.0	278	1 TDRTOX	OX-2 membrane glyco
31	162.5	6.0	858	1 IURTC	neural cell adhesi
32	162	6.0	587	2 JH0464	DM-GRASP precursor
33	162	6.0	761	1 JH0464	neural cell adhesi
34	162	6.0	765	2 A42632	cell adhesion mole
35	162	6.0	812	2 A42632	cell adhesion mole
36	162	6.0	932	2 A42632	cell adhesion mole
37	161.5	6.0	739	2 JH0581	vascular cell adhe
38	160.5	5.9	702	2 A36319	carcinoembryonic a
39	160	5.9	725	1 JMSNG	neural cell adhesi
40	157	5.8	509	2 JCS288	SHP substrate-1 pr
41	157	5.8	1091	1 IYCHN1	neural cell adhesi
42	156	5.8	646	2 I38049	cell surface glyco
43	155	5.7	513	2 JCS289	SHP substrate-1 pr
44	154	5.7	1612	2 J30805	ductil protein - mo
45	153.5	5.7	1051	2 A39712	kinase-like protei

ALIGNMENTS

RESULT 1
T08732
hypothetical protein DKFZ566B0846.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C:Accession: T08732
R/Ottewill, B.; Obermayer, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16474
A:Accession: T08732
A:Molecule type: mRNA
A:Residues: 1-407 <OTT>
A:Cross-references: EMBL:AL050071
A:Experimental source: fetal kidney; clone DKFZ566B0846
C:Genetics:
A>Note: DKFZ566B0846.1

Query Match 43.3%; Score 1173.5; DB 2; Length 407;
Best Local Similarity 62.8%; Pred. No. 5.8e-79;
Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7;

QY	143	SGKTCVAVTPPLNAAOSTTTTVLVEPTVSLIKGPDLSLDGNETVAALCIATGKVA	202
DB	1	SGKTCVAVTPPLNAAOSTTTTVLVEPTVSLIKGPDLSLDGNETVAALCIATGKVA	60
QY	203	HIDWEGDLGEMESTTTSFVETATIIISQKLPTRFARGRIRICVAGHPALBKDIRYSFI	262
DB	61	HIDWEGDLGEMESTTTSFVETATIIISQKLPTRFARGRIRICVAGHPALBKDIRYSFI	120
QY	263	LIDVAPAVSVTVGVGNMFWGRKYNLKNADANPPFKVWGRIDGQWPDLSADNTL	322
DB	121	LIDVAPAVSVTVGVGNMFWGRKYNLKNADANPPFKVWGRIDGQWPDLSADNTL	180
QY	323	HFVHPLTVNYSVYICVNTSLGORSQKVYIISDV	359
DB	181	HFVHPLTVNYSVYICVNTSLGORSQKVYIISDV	240
QY	360	FKQTSINAGAVIGAVLAFITAVTVLTPRK--RPSYLDKV	403
DB	241	ERKQPLPLSLATIKDITATIASVVGALPIVLVSVLAGIPICTRRKRTGRGYPKRN	300
QY	404	IDLPETH-----KPPLYERSPLPFOKDLFQDEH--PLQTFKEREVNG	446
DB	301	Y-IPSDMQKESQIDVLQDELDPYDQVKKENKPNVNLIRDYLEBPEKTOW-----N	354
QY	447	NLQHSNGLSRSPDYDENPVG	468
DB	355	NVENINRF-ERPMVDYEDLKMVG	375

RESULT 2
JC4024

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OM protein - protein search, using SW model

Run on: December 15, 2002, 09:04:27 / Search time 14.7051 Seconds
(without alignments)
3354.117 Million cell updates/sec

Title: US-09-972-268-12

Perfect score: 2707

Sequence: 1 MARTLRPSPLCPGSGKKAQLS.....KHQNNPKKVVYIDPRHHV 510

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: PIR_73:1*
2: PIR_73:2*
3: PIR_73:3*
4: PIR_73:4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1173.5	43.4	407	2 T08732	hypothetical prote
2	565.5	20.9	518	2 JC4024	poliovirus recepto
3	540	19.9	530	2 A53437	poliovirus recepto
4	527	19.5	538	2 I68093	PR2 delta - human
5	467	17.3	467	1 HLMSP3	poliovirus recepto
6	455	16.8	478	2 I53960	PR2 alpha - human
7	418	15.4	392	2 B44194	poliovirus recepto
8	418	15.4	417	2 B44194	poliovirus recepto
9	402	14.9	392	1 RHMUPD	poliovirus recepto
10	402	14.9	392	1 RHMUPD	poliovirus recepto
11	326.5	12.1	417	1 RHMUPD	poliovirus recepto
12	229.5	8.5	764	2 A54017	poliovirus recepto
13	203.5	7.6	4391	2 A54017	colon carcinoma-as
14	196.5	7.3	5195	2 A58096	irregular chiasm C
15	196.5	7.3	5195	2 T20992	hypothetical prote
16	187.5	6.9	274	2 T23290	hemitecint precurs
17	187.5	6.9	274	2 A47639	OX-2 membrane glyc
18	178.5	6.6	3707	2 T08851	Down syndrome cell
19	178	6.6	588	2 JH0506	heparan sulfate pr
20	178	6.6	588	2 JH0506	heparan sulfate pr
21	177.5	6.6	853	2 A45254	surface glycoprote
22	177	6.5	626	1 A61084	neural cell adhesi
23	177	6.5	637	2 B33785	myelin-associated
24	176	6.5	7962	2 I38346	elastic titin - hu
25	175	6.5	582	1 BNR13	myelin-associated
26	175	6.5	626	1 BNR13	myelin-associated
27	174	6.4	1091	2 A58532	glial cell membra
28	170.5	6.3	365	2 JC7780	coxsackie- and ade
29	164.5	6.1	847	2 JH0371	B-cell adhesion pr

30	162.5	6.0	278	1 TDRTOX	OX-2 membrane gly
31	162.5	6.0	858	1 IJRTNC	neural cell adhesi
32	162	6.0	587	2 JH0464	DM-GRASP precursor
33	162	6.0	761	1 IJHUNG	neural cell adhesi
34	162	6.0	765	2 C42632	cell adhesion mole
35	162	6.0	812	2 B42632	cell adhesion mole
36	162	6.0	932	2 A42632	cell adhesion mole
37	161.5	6.0	739	2 JH0581	vascular cell adhe
38	160.5	5.9	702	2 A56319	carcinoembryonic a
39	160	5.9	725	1 IJMSNG	neural cell adhesi
40	157	5.8	509	2 JC5288	SHP substrate-1 pr
41	157	5.8	1091	1 IJCHNL	neural cell adhesi
42	156	5.8	646	2 I38049	cell surface glyco
43	155	5.7	513	2 JC5289	SHP substrate-1 pr
44	154	5.7	1612	2 T30805	ductal protein - mo
45	153.5	5.7	1051	2 A39712	kinase-like protei

ALIGNMENTS

RESULT 1

T08732

hypothetical protein DKF2p566B0846.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999

C:Accession: T08732

R:O'Brienwelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16474

A:Accession: T08732

A:Molecule type: mRNA

A:Residues: 1-407 <OT>

A:Cross-references: EMBL:AL050071

A:Experimental source: fetal kidney; clone DKF2p566B0846

C:Genetics:

A:Note: DKF2p566B0846.1

Query Match

Best Local Similarity 43.4%; Score 1173.5; DB 2; Length 407;

Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7;

QY	143	SGKTKCAVTPPLGNAOSSTTVTVLVEFTVSLIKGPDSLIDGNETVAICTAATGKPA	202
DB	1	SGKTKCAVTPPLGNAOSSTTVTVLVEFTVSLIKGPDSLIDGNETVAICTAATGKPA	60
QY	203	HIDWEGDGESESTTTSFPNETATIIISQYKLPTRFARGRRTICVAKPALCKDIRSFI	262
DB	61	HIDWEGDGESESTTTSFPNETATIIISQYKLPTRFARGRRTICVAKPALCKDIRSFI	120
QY	263	LIDQYAPREVSTGVDGWMFYGRKYNLKNADANPPPKSVSRUDGOMPGLASDNTL	322
DB	121	LIDQYAPREVSTGVDGWMFYGRKYNLKNADANPPPKSVSRUDGOMPGLASDNTL	180
QY	323	HFVAPLTVNSGVITCKVNTSLAQSRDOKVYISDVP-----	359
DB	181	HFVAPLTVNSGVITCKVNTSLAQSRDOKVYISDPTTTTLOPTIOMHPTADIEDLAT	240
QY	360	-----FKOTSSIAVAGVIGAVLAFIAIFVTVLTPRK--RPSYLDKV	403
DB	241	EPKUPPLPLSTLATIKODTITATIASVVGALPIVAVSLAGIFCVRARRTRRGDYAKN	300
QY	404	IDLPPH-----KPPPLVEHRSPPLPKDLFGQEH--PLQGFKEHVG	446
DB	301	Y-IPSDMQKESQIDVLCQDELDPIDSVKKNKPNVNNLIRKDYISEPKTQM-----N	354
QY	447	NLOHNSGINSRSPFYEDENPVG	468
DB	355	NVENLIRF-ERPMDYEDLMG	375
RESULT 2		JC4024	



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OM protein - protein search, using sw model

Run on: December 15, 2002, 09:04:27 : Search time 15.6278 Seconds
(without alignments)
3334.117 Million cell updates/sec

Title: US-09-972-268-2

Perfect score: 1 SPICPGCKAKQLSSASLGLA.....EDDLVSHVDSVTSRRKRV 542

Sequence: BLOSUM62

Scoring table: GAPOP 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

1 number of hits satisfying chosen parameters: 283224

Maximum DB seq length: 0,
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR.73.*
2: PIR1.*
3: PIR2.*
4: PIR3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2141	74.7	407	2 T08732	hypothetical prote
2	627	21.9	518	2 UC4024	poliovirus recepto
3	494	17.2	467	1 HLMSP3	poliovirus recepto
4	470	16.4	530	2 A53437	poliovirus recepto
5	463.5	16.2	478	2 I53960	PRR2 alpha - human
6	449.5	15.7	538	2 I68093	PRR2 delta - human
7	422.5	14.7	417	2 A44194	poliovirus recepto
8	415.5	14.5	392	2 B44194	poliovirus recepto
9	390.5	13.6	392	1 RMTUPD	poliovirus recepto
10	390.5	13.6	417	1 RMTUPD	poliovirus recepto
11	331.5	11.6	416	2 A54017	poliovirus recepto
12	230.5	8.0	764	2 A49448	colon carcinoma-as
13	215.5	7.5	4391	2 A38096	irregular Chlam C
14	201	7.0	5175	2 T20992	perlecan precursor
15	201	7.0	5198	2 T43290	hypothetical prote
16	198	6.9	588	2 JH0506	hemolysins prote
17	194	6.8	588	2 JH0506	adhesion molecule
18	189	6.6	853	1 IJBONC	surface glycoprote
19	187.5	6.5	274	2 A47639	neural cell adhesi
20	187.5	6.5	7962	2 I38346	OX-2 membrane glyc
21	182	6.4	587	2 JH0464	elastic titin - hu
22	181.5	6.3	1896	2 JH0851	DM-GRASP precursor
23	178.5	6.2	847	2 JH0371	Down syndrome cell
24	177	6.2	3707	2 S18252	B-cell adhesion pr
25	174	6.1	858	1 IJUNNG	heparan sulfate pr
26	173.5	6.1	761	1 IJUNNG	neural cell adhesi
27	173	6.0	637	2 JCS785	myelin-associated
28	172	6.0	513	2 JCS289	SHP substrate-1 pr
29	171.5	6.0	822	2 B49151	fibroblast growth

30	171	6.0	458	2 S23699	cell-adhesion mole
31	171	6.0	582	1 ENRT3S	myelin-associated
32	171	6.0	626	1 ENRT3S	myelin-associated
33	171	6.0	1259	2 A43425	Bravo/Mr-CAM cell
34	169.5	5.9	1091	1 IJCHNL	neural cell adhesi
35	169	5.9	765	2 C42632	myelin-associated
36	168	5.9	812	2 B42632	cell adhesion mole
37	168	5.9	932	2 A42632	cell adhesion mole
38	168	5.8	822	2 S19947	cell adhesion mole
39	166.5	5.8	822	2 S19947	fibroblast growth
40	166	5.8	739	2 JN0581	vascular cell adhe
41	165	5.8	725	1 JN0581	neural cell adhesi
42	165	5.8	1115	1 JN0581	neural cell adhesi
43	164.5	5.7	569	2 A46462	T cell activation
44	164	5.7	521	2 JCL1508	biliary glycoprote
45	163	5.7	458	1 WMSKRL	biliary glycoprote

ALIGNMENTS

RESULT 1
T08732
Hypothetical protein DKFZ566B0846.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999-#text_change 13-Aug-1999
C/Accession: T08732
R/Ottensmeyer, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A/Reference number: Z16474
A/Accession: T08732
A/Molecule type: mbpa
A/Residues: 1-407<OT>
A/Cross-references: EMBL:AL050071
A/Experimental source: fetal kidney; clone DKFZ566B0846
A/Genetics:
A/Note: DKFZ566B0846.1

Query Match 74.7%; Score 2141; DB 2; Length 407;
Best local similarity 99.3%; Pred. No. 3.7e-145;
Matches 404; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	136	SGKTCAGVPPGKNOSSSTVTVLVEPTVSLKGPDSLTCGNETVAALCIATGKPPVA	195
DB	1	SGKTCAGVPPGKNOSSSTVTVLVEPTVSLKGPDSLTCGNETVAALCIATGKPPVA	60
QY	196	HIDWEGDLGEMESTTSPFNPTATIIISOYLPPTFRFARGRITTCVVKHPALEKDIRSFI	255
DB	61	HIDWEGDLGEMESTTSPFNPTATIIISOYLPPTFRFARGRITTCVVKHPALEKDIRSFI	120
QY	256	LDIYAPFVSVTGQGNFVGRKGVNLCNADANPPFESVWSRLDQMPGSLASDNTL	315
DB	121	LDIYAPFVSVTGQGNFVGRKGVNLCNADANPPFESVWSRLDQMPGSLASDNTL	180
QY	316	HFVHPLTFNYSGYIKCTYNSLIGRSDOKTIIYSDPTTTTLOPTIOHNSDIEDLAT	375
DB	181	HFVHPLTFNYSGYIKCTYNSLIGRSDOKTIIYSDPTTTTLOPTIOHNSDIEDLAT	240
QY	376	EPKCLPPLSTLTIKDTIATIIASVGGALFTIVSVLAGIFCYRRRTFRDGFAYN	435
DB	241	EPKCLPPLSTLTIKDTIATIIASVGGALFTIVSVLAGIFCYRRRTFRDGFAYN	300
QY	436	YIPSPDMQKSOIDVLCQDELDPYDSVKKENPNNILRDVLEBEKQNNVENNL	495
DB	301	YIPSPDMQKSOIDVLCQDELDPYDSVKKENPNNILRDVLEBEKQNNVENNL	360
QY	496	RFRPMDYEDLNMGRFVSDHYNEDDLVSHVDGSVTSRRKRV 542	
DB	361	RFRPMDYEDLNMGRFVSDHYNEDDLVSHVDGSVTSRRKRV 407	

RESULT 2
JC4024



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OM protein - protein search, using sw model

Run on: December 15, 2002, 09:04:27 ; Search time 28.4142 Seconds
(without alignments)
3930.349 Million cell updates/sec

Title: US-09-972-268-2

Perfect score: 2866
Sequence: 1 SPLPCGGKRAQLSSASLILGA.....ENDLIVSHVGSVSRREMY 542

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 20604715 residues

1 number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2866	100.0	549	4 Q9N0S3	Q9N0S3 homo sapien
2	2700	94.2	549	11 Q9JLB9	Q9JLB9 mus musculu
3	2656	92.7	549	11 Q9D006	Q9D006 mus musculu
4	2141	74.7	407	4 Q9Y412	Q9Y412 homo sapien
5	1793.5	62.6	510	11 Q9JLB8	Q9JLB8 mus musculu
6	1788.5	62.4	438	11 Q9JLB7	Q9JLB7 mus musculu
7	1629	56.8	304	4 Q9BVA5	Q9BVA5 homo sapien
8	544	19.0	510	4 Q9BVA5	Q9BVA5 homo sapien
9	543	18.9	510	4 Q9BVA5	Q9BVA5 homo sapien
10	542	18.9	101	4 Q9BVA5	Q9BVA5 homo sapien
11	534.5	18.6	295	11 Q9BVA5	Q9BVA5 masocricetu
12	528	18.4	298	6 Q9GL74	Q9GL74 ceropithec
13	526.5	18.4	295	6 Q9GL75	Q9GL75 bos taurus
14	506	17.7	508	11 Q9C007	Q9C007 mus musculu
15	496	17.3	99	11 Q9C007	Q9C007 mus musculu
16	494	17.2	467	11 Q91V79	Q91V79 mus musculu

17	493.5	17.2	463	11 Q9DBE8	Q9DBE8 mus musculu
18	432	15.1	449	4 Q9UB16	Q9UB16 homo sapien
19	413.5	14.4	412	11 Q9B1E1	Q9B1E1 ratius norv
20	408.5	14.3	412	11 Q9B1E1	Q9B1E1 ratius norv
21	400.5	14.0	401	6 Q9B835	Q9B835 ceropithec
22	393	13.7	408	11 Q91W1	Q91W1 mus musculu
23	390.5	13.6	417	4 Q9B8J1	Q9B8J1 homo sapien
24	346	12.1	415	11 Q9C077	Q9C077 mus musculu
25	337	11.8	494	11 Q9C073	Q9C073 mus musculu
26	336.5	11.7	456	11 Q9B5W8	Q9B5W8 mus musculu
27	334.5	11.7	442	4 Q9B1E7	Q9B1E7 homo sapien
28	334	11.7	445	11 Q9B4L1	Q9B4L1 mus musculu
29	271.5	9.5	336	11 Q9B6T7	Q9B6T7 mus musculu
30	250	8.7	261	11 Q9D6A9	Q9D6A9 mus musculu
31	247	8.6	396	11 Q9N28	Q9N28 mus musculu
32	234	8.2	959	5 Q9N9Y9	Q9N9Y9 drosophila
33	234	8.2	968	5 Q9W4T9	Q9W4T9 drosophila
34	233	8.1	306	11 Q9C0Y4	Q9C0Y4 mus musculu
35	232	8.1	432	4 Q9J1P1	Q9J1P1 homo sapien
36	229.5	8.0	975	5 Q9J1T4	Q9J1T4 drosophila
37	226.5	7.9	295	11 Q9QY16	Q9QY16 mus musculu
38	226.5	7.9	295	11 Q9Z2H8	Q9Z2H8 mus musculu
39	218	7.6	278	11 Q9QYU3	Q9QYU3 mus musculu
40	216	7.5	345	5 Q9W4U1	Q9W4U1 drosophila
41	215.5	7.5	4370	4 Q9H3V5	Q9H3V5 homo sapien
42	212.5	7.4	289	11 Q9QY15	Q9QY15 mus musculu
43	209	7.3	388	11 Q9R4E4	Q9R4E4 mus musculu
44	209	7.3	509	11 Q9C0W5	Q9C0W5 ratius norv
45	207	7.2	509	11 P97710	P97710 ratius norv

ALIGNMENTS

RESULT 1
ID Q9N0S3 PRELIMINARY; PRT; 549 AA.

AC Q9N0S3: 01-OCT-2000 (TRENBERG, 15, Created)
DT 01-OCT-2000 (TRENBERG, 15, Last sequence update)
DT 01-DEC-2001 (TRENBERG, 15, Last annotation update)
DE Nectin 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Raymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,
RT Dubreuil P., Lopez M.;
RT "Human nectin 3/PR3: A novel member of the PVN/PRN/nectin family that
RT interacts with afadin."
RL Gene 0:0-0(2000)
DR EMBL; AF282874; AAP9757.1; -
DR InterPro; IPR003599; Ig
DR InterPro; IPR003600; Ig_1ike.
DR InterPro; IPR003006; Ig_1MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; Ig_1like; 1.
SQ SEQUENCE 549 AA; 6100 MW; 6D1104CBA8D731 CRC64;

Query Match 100.0%; Score 2866; DB 4; Length 549;
Best local similarity 100.0%; Pred. No. 4.3e-217; Indels 0; Gaps 0;
Matches 542; Conservative 0; Mismatches 0;

QY 1 SPLPCGGKRAQLSSASLILGAGLLQPTPLILLPLLLFSRLCGALAGPIIVEPHT 60
DB 8 SPLPCGGKRAQLSSASLILGAGLLQPTPLILLPLLLFSRLCGALAGPIIVEPHT 67
QY 61 AVMKQNVSKLIEVFETITQISWEKHGKSGQYAVVHPQYGSVQGEYQGVLEPKYNS 120
DB 68 AVMKQNVSKLIEVFETITQISWEKHGKSGQYAVVHPQYGSVQGEYQGVLEPKYNS 127

QY 121 LNDATITLHNIIGFSDSGKYICKAVTFFPLGNAQSSSTTVTLVEPTVSLIKGPDSLIDGNE 180
 DB 128 LNDATITLHNIIGFSDSGKYICKAVTFFPLGNAQSSSTTVTLVEPTVSLIKGPDSLIDGNE 187
 QY 181 TVAAICIAATGKPVAHIDWEGDLGEMESTTTFSPNETATIIISQYKLPFTRFARGRRITCV 240
 DB 188 TVAAICIAATGKPVAHIDWEGDLGEMESTTTFSPNETATIIISQYKLPFTRFARGRRITCV 247
 QY 241 VGHPALEKDIRYSFILDIOYAPEVSVTVGDNWFGVGRKGVNLKCNADANPPFPKSVWSRL 300
 DB 248 VGHPALEKDIRYSFILDIOYAPEVSVTVGDNWFGVGRKGVNLKCNADANPPFPKSVWSRL 307
 QY 301 DGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTTTTLOPT 360
 DB 308 DGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTTTTLOPT 367
 QY 361 IQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFVLVSVLAGIFC 420
 DB 368 IQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFVLVSVLAGIFC 427
 QY 421 YRRRTFRGDFYAKYIIPSDMQESQIDVLQDELDSPDSVKENKPNVNLIRKDYL 480
 DB 428 YRRRTFRGDFYAKYIIPSDMQESQIDVLQDELDSPDSVKENKPNVNLIRKDYL 487
 QY 481 EPEKTQWNNVNLNRFERPMYEDLKMGMKFPVSDHYDENEDLVSHVDGVSISRREW 540
 DB 488 EPEKTQWNNVNLNRFERPMYEDLKMGMKFPVSDHYDENEDLVSHVDGVSISRREW 547
 QY 541 YV 542
 DB 548 YV 549

RESULT 2

Q9JLB9 ID Q9JLB9 PRELIMINARY; PRT; 549 AA.
 AC Q9JLB9
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE Cell adhesion molecule nectin-3 alpha.
 GN PVRL3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20209403; PubMed=10744716;
 RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
 Tachibana K., Mizoguchi A., Takai Y.;
 RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
 RT that shows homophilic and heterophilic cell-cell adhesion
 RT activities";
 RL J. Biol. Chem. 275:10291-10299 (2000).
 DR EMBL; AF195833; AAF63685.1; -.
 DR MGD; MGI:1950171; Pvr13.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003600; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; ig_2.
 DR SMART; SM00409; IG_1.
 DR SMART; SM00410; IG-like; 1.
 SO SEQUENCE 549 AA; 60583 MW; 5492C9A8B472F195 CRC64;
 Query Match 94.24; Score 2700; DB 11; Length 549;
 Best Local Similarity 93.24; Pred. No. 5e-204;
 Matches 505; Conservative 19; Mismatches 18; Indels 0; Gaps 0;
 QY 1 SPLCPGGKQAQSSASLGLGILLQPPPTPPPLLLLLFPILLFSLRCLGALAGPIIVEPHT 60
 DB 8 APLCPGGKQAQSSAAPPAAQLLPAPTPPPPLLLLLFPILLFSLRCLGALAGPIIVEPHT 67

QY 61 AVWGRKNSLKLLEVNNETLTQISWEKIHGKSSQTVAVHHPQYGFSGVEYQGRVLPKNYS 120
 DB 69 AVWGRKNSLKLLEVNNETLTQISWEKIHGKSTQTVAVHHPQYGFSGVEYQGRVLPKNYS 127
 QY 121 LNDATITLHNIIGFSDSGKYICKAVTFFPLGNAQSSSTTVTLVEPTVSLIKGPDSDIDGNE 180
 DB 128 LNDATITLHNIIGFSDSGKYICKAVTFFPLGNAQSSSTTVTLVEPTVSLIKGPDSDIDGNE 187
 QY 181 TVAAICIAATGKPVAHIDWEGDLGEMESTTTFSPNETATIIISQYKLPFTRFARGRRITCV 240
 DB 188 TVAAICIAATGKPVAHIDWEGDLGEMESTTTFSPNETATIIISQYKLPFTRFARGRRITCV 247
 QY 241 VGHPALEKDIRYSFILDIOYAPEVSVTVGDNWFGVGRKGVNLKCNADANPPFPKSVWSRL 300
 DB 248 VGHPALEKDIRYSFILDIOYAPEVSVTVGDNWFGVGRKGVNLKCNADANPPFPKSVWSRL 307
 QY 301 DGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTTTTLOPT 360
 DB 308 DGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTTTTLOPT 367
 QY 361 IQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFVLVSVLAGIFC 420
 DB 368 IQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFVLVSVLAGIFC 427
 QY 421 YRRRTFRGDFYAKYIIPSDMQESQIDVLQDELDSPDSVKENKPNVNLIRKDYL 480
 DB 428 YRRRTFRGDFYAKYIIPSDMQESQIDVLQDELDSPDSVKENKPNVNLIRKDYL 487
 QY 481 EPEKTQWNNVNLNRFERPMYEDLKMGMKFPVSDHYDENEDLVSHVDGVSISRREW 540
 DB 488 EPEKTQWNNVNLNRFERPMYEDLKMGMKFPVSDHYDENEDLVSHVDGVSISRREW 547
 QY 541 YV 542
 DB 548 YV 549
 RESULT 3
 Q9D006 ID Q9D006 PRELIMINARY; PRT; 549 AA.
 AC Q9D006
 DT 01-JUN-2001 (TREMELrel. 17, Created)
 DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
 DE 2610301B19Rik protein.
 GN 2610301B19Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J; TISSUE=EMBRYO;
 RC MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 Schram L.M., Straubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 Gunsberg S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 Hayaashizaki Y.,

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OM protein - protein search, using sw model

Run on: December 15, 2002, 09:04:27 ; Search time 12.6003 Seconds
(without alignment)
3334.117 Million cell updates/sec

Title: US-09-972-268-31

Perfect score: 2299

Sequence: 1 MARTLRPSPLCPGSGKAQLS.....ERSPLPDKDLFCVCHVEYT 437

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73.*
2: PIR1.*
3: PIR2.*
4: PIR3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1159.5	50.4	407	2 T08732	hypothetical prote
2	544	23.7	518	2 JC4024	poliovirus recepto
3	495.5	21.6	530	2 A53437	poliovirus recepto
4	490	21.3	538	2 I68093	PR2 delta - human
5	467	20.3	467	1 HLMSP3	poliovirus recepto
6	455	19.8	478	2 I53960	PR2 alpha - human
7	418	18.2	392	2 B44194	poliovirus recepto
8	418	18.2	417	2 A44194	poliovirus recepto
9	402	17.5	392	1 RMHUPD	poliovirus recepto
10	402	17.5	417	2 A44194	poliovirus recepto
11	326.5	14.2	416	2 A54017	poliovirus recepto
12	229.5	10.0	764	2 A49448	colon carcinoma-as
13	205.5	8.9	4391	2 A38096	irregular chlam C
14	196.5	8.5	5175	2 T20992	perlecan precursor
15	196.5	8.5	5198	2 T20992	hypothetical prote
16	187.5	8.2	274	2 A47639	hemocytin precurs
17	178	7.7	588	2 JH0506	OK-2 membrane glye
18	178	7.7	588	2 A45254	adhesion molecule
19	177.5	7.7	853	2 A45254	surface glycoprote
20	177	7.7	626	1 JUBONC	neural cell adhesi
21	177	7.7	637	2 -B33785	myelin-associated
22	176	7.7	7962	2 I36346	elastic titin - hu
23	175	7.6	582	1 BNR738	myelin-associated
24	175	7.6	626	1 BNR73	myelin-associated
25	174.5	7.6	1896	2 T08851	Down syndrome cell
26	173.5	7.5	3707	2 S18252	heparan sulfate pr
27	171	7.4	1091	2 A58532	glial cell membran
28	170.5	7.4	365	2 JCT780	coxsackie- and ade
29	164.5	7.2	847	2 JH0371	B-cell adhesion pr

30	162.5	7.1	278	1 TDRTOX	OX-2 membrane glye
31	162.5	7.1	858	1 J0RTWC	neural cell adhesi
32	162	7.0	587	2 JH0464	DN-GRASP precursor
33	162	7.0	761	1 JHUNG	neural cell adhesi
34	162	7.0	765	2 C42632	cell adhesion mole
35	162	7.0	812	2 B42632	cell adhesion mole
36	162	7.0	702	2 A42632	cell adhesion mole
37	160.5	7.0	702	2 A42632	cell adhesion mole
38	157	6.8	739	2 JH0381	carcinoembryonic a
39	157	6.8	1091	1 JUCHNL	vascular cell adhe
40	156	6.8	646	2 I38049	neural cell adhesi
41	154.5	6.7	509	2 JCS288	cell surface glyco
42	154	6.7	1612	2 T30805	SHP substrate-1 pr
43	153.5	6.7	725	1 IJMSNG	ductil protein - mo
44	153.5	6.7	1115	1 IJMSNG	neural cell adhesi
45	153	6.7	1051	2 A39712	kinase-like protei

ALIGNMENTS

RESULT 1
T08732
hypothetical protein DKFZ566B0846.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C/Accession: T08732
R/Octenwelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16474
A:Accession: T08732
A:Molecule type: mRNA
A:Residues: 1-407 <OTT>
A:Cross-references: EMBL:AL050071
A:Experimental source: fetal kidney; clone DKFZ566B0846
C/Genetics:
A/Note: DKFZ566B0846.1

Query Match 50.4%, Score 1159.5, DB 2, Length 407;
Best Local Similarity 70.3%, Pred. No. 9.1e-78;

Matches 230; Conservative 16; Mismatches 32; Indels 49; Gaps 4;

QY	143	SSKYICAKVTPLGNAOSSSTTVTVLVEPTVSLIKGPSLIDGNETVAICIAATGPRVA	202
DB	1	SSKYICAKVTPLGNAOSSSTTVTVLVEPTVSLIKGPSLIDGNETVAICIAATGPRVA	60
QY	203	HTDMSGDLMGEMSTTSPFNETATIIIOYKLPFRFARGRIITCVKHPALEKDIRSFI	262
DB	61	HTDMSGDLMGEMSTTSPFNETATIIIOYKLPFRFARGRIITCVKHPALEKDIRSFI	120
QY	263	LDIOYABEVSVTGYDGNMFVGRGVNIKCNADANPPPKSVMSRLDQMPDGLASDNTL	322
DB	121	LDIOYABEVSVTGYDGNMFVGRGVNIKCNADANPPPKSVMSRLDQMPDGLASDNTL	180
QY	323	HEVHPLFNTSGVYICKVTNSLQGRSDOKVYISDVP-----	359
DB	181	HEVHPLFNTSGVYICKVTNSLQGRSDOKVYISDVP-----	240
QY	360	-----FQGSIVAGAVGAVLAFIATFVLLTPRK--RPSYLDKV	403
DB	241	BEKKLPPLSTLATITDVTIATIVSVGALFTVLSVLAGFCYRRRRTRFDYPAK-	299
QY	404	IDLPEPTKPPPLYSERSPLPDKLFCQ	430
DB	300	-----NYIPPSDMQKES-----QIDVLQ	317

RESULT 2
JC4024
poliovirus receptor-related protein precursor - human
C/Species: Homo sapiens (man)
C/Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C/Accession: JC4024

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OM protein - protein search, using SW model

Run on: December 15, 2002, 09:39:57 ; Search time 21 seconds

(without alignments)
2513.228 Million cell updates/sec

Title: US-09-972-268-4

Sequence: 1 MARTPSPPLCGGKAGLS.....EDLVSHVDGVSIRREMY 549

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Maximum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:*

1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2141	73.7	407	2 T08732	hypothetical prote
2	627	21.6	518	2 JC4024	poliovirus recepto
3	494	17.0	467	1 HLMP3	poliovirus recepto
4	470	16.2	530	2 A53437	poliovirus recepto
5	463.5	16.0	478	2 I53960	PRR2 alpha - human
6	449.5	15.5	538	2 I58093	poliovirus recepto
7	422.5	14.5	417	2 A44194	poliovirus recepto
8	415.5	14.3	392	2 B44194	poliovirus recepto
9	390.5	13.4	392	1 RWH0PD	poliovirus recepto
10	390.5	13.4	417	1 RWH0PD	poliovirus recepto
11	331.5	11.4	416	2 A54017	colon carcinoma-as
12	230.5	7.9	764	2 A49448	irregular chlam C
13	215.5	7.4	4391	2 A38096	perlecan precursor
14	201	6.9	5175	2 T20992	hypothetical prote
15	201	6.9	5198	2 T43290	hemifuscin precurs
16	198	6.8	588	2 JH0506	adhesion molecule
17	194	6.7	588	2 A45254	surface glycoprote
18	189	6.5	853	1 JH08C	neural cell adhesi
19	187.5	6.5	274	2 A47639	OX-2 membrane gly
20	187.5	6.5	7962	2 I36346	elastic titin - hu
21	182	6.3	587	2 JH0464	DM-GRASP precursor
22	181.5	6.2	1896	2 T08851	Down syndrome cell
23	179	6.2	3707	2 S18252	heparan sulfate pr
24	178.5	6.1	847	2 JH0371	B-cell adhesion pr
25	174	6.0	858	1 JH08C	neural cell adhesi
26	173.5	6.0	761	1 JH08C	neural cell adhesi
27	173	6.0	637	2 B31785	myelin-associated
28	172	5.9	832	2 UC5289	SHP substrate-1 pr
29	171.5	5.9	822	2 B49151	fibroblast growth

30	171	5.9	458	2 S23969	cell-adhesion mole
31	171	5.9	582	1 BNR73	myelin-associated
32	171	5.9	626	1 BNR73	myelin-associated
33	171	5.9	1259	2 A43425	Bravo/Nr-CAM cell
34	169.5	5.8	1091	1 JH08C	neural cell adhesi
35	169	5.8	626	1 A61084	myelin-associated
36	168	5.8	765	2 C42632	cell adhesion mole
37	168	5.8	812	2 B42632	cell adhesion mole
38	168	5.8	932	2 A42632	cell adhesion mole
39	166.5	5.7	822	2 S19947	fibroblast growth
40	166	5.7	739	2 JH0581	vascular cell adhe
41	165	5.7	725	1 JH0581	neural cell adhesi
42	165	5.7	1115	1 JH0581	neural cell adhesi
43	164.5	5.7	569	2 A46462	T cell activation
44	164	5.6	521	2 UC1508	biliary glycoprote
45	163	5.6	458	1 WMSR1	biliary glycoprote

ALIGNMENTS

RESULT 1

T08732 hypothetical protein DKFZ566B0846.1 - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999

C/Accession: T08732

R/Oltenswelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999

A/Reference number: Z16474

A/Accession: T08732

A/Molecule type: mRNA

A/Residues: 1-407 <OTT>

A/Cross-References: EMBL:AL050071

A/Experimental source: Fetal kidney; clone DKFZ566B0846

C/Genetics:

A/Note: DKFZ566B0846.1

Query Match 73.7% Score 2141; DB 2; Length 407;

Best Local Similarity 99.3%; Pred. No. 3.7e-145; Matches 404; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	143	SGKTYCAVTPPLGNQSTTTVTVVEPTVSLIKGPDSLIDGNETVAICIAATGKPYA	202
DB	1	SKYICAVTVFPPLGNQSTTTVTVVEPTVSLIKGPDSLIDGNETVAICIAATGKPYA	60
QY	203	HIWEGDLGEMSTTSPFNETATIIISQKLFPTPRFARGRITCVVKPALEKDIRSFI	262
DB	61	HIWEGDLGEMSTTSPFNETATIIISQKLFPTPRFARGRITCVVKPALEKDIRSFI	120
QY	263	LDIQAPBVSTYGDGNWFRVGRKYNLKCNDANPPFPFSSVWSRLDQWPGGLASDNTL	322
DB	121	LDIQAPBVSTYGDGNWFRVGRKYNLKCNDANPPFPFSSVWSRLDQWPGGLASDNTL	180
QY	323	HFVHPLTFNSGYVYICKVNLSIGRSQKVIYISDPPTTTLOPTIOHMPSTADIEDLAT	382
DB	181	HFVHPLTFNSGYVYICKVNLSIGRSQKVIYISDPPTTTLOPTIOHMPSTADIEDLAT	240
QY	383	REKXLPPLSTLANTINDDTIATITISVGGALFTVYSVLAGIFCRRRRPRGRDPAKN	442
DB	241	REKXLPPLSTLANTINDDTIATITISVGGALFTVYSVLAGIFCRRRRPRGRDPAKN	300
QY	443	YIPPEMQKSSQIDVLQODELSDYPDSYKKNKXPNVNLIRDYLEEPKTOHNVNENLN	502
DB	301	YIPPEMQKSSQIDVLQODELSDYPDSYKKNKXPNVNLIRDYLEEPKTOHNVNENLN	360
QY	503	REPRMDYEDLQMGKRFVSDSHYDENEDLVSHVDGVSIRREMY 549	
DB	361	REPRMDYEDLQMGKRFVSDSHYDENEDLVSHVDGVSIRREMY 407	

RESULT 2
JC4024



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OM protein - protein search, using sw model

Run on: December 15, 2002, 09:04:27 / Search time 14.5321 Seconds

(without alignments)
3334.117 Million cell updates/sec

Title: US-09-972-268-8

Perfect score: 2679
Sequence: 1 PSPICPGGKAKQSSASLIG.....KHQNDPKKVIIDPREHY 504

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: 1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1173.5	43.8	407	2 T08732	hypothetical prote
2	565.5	21.1	518	2 UC4024	poliovirus recepto
3	540	20.2	530	2 A53437	poliovirus recepto
4	527	19.7	538	2 I68093	PRR2 delta - human
5	467	17.4	467	1 HLMSP3	poliovirus recepto
6	455	17.0	478	2 I53960	PRR2 alpha - human
7	418	15.6	392	2 B44194	poliovirus recepto
8	418	15.6	417	2 A44194	poliovirus recepto
9	402	15.0	392	1 RWHUPD	poliovirus recepto
10	402	15.0	417	1 RWHUPD	poliovirus recepto
11	326.5	12.2	416	2 A54017	poliovirus recepto
12	229.5	8.6	764	2 A49448	colon carcinoma-as
13	204.5	7.6	4391	2 A38096	irregular chain C
14	196.5	7.3	5175	2 T20992	perlecan precursor
15	196.5	7.3	5198	2 T43290	hypothetical prote
16	187.5	7.0	274	2 A47639	hemocytin precurs
17	181.5	6.8	1896	2 T08851	OX-2 membrane glyc
18	178	6.6	588	2 JH0506	down syndrome cell
19	178	6.6	588	2 A45254	adhesion molecule
20	177.5	6.6	853	1 IUBONC	surface glycoprote
21	177	6.6	626	1 A61084	neutral cell adhesi
22	177	6.6	637	2 B33785	myelin-associated
23	176	6.6	7962	2 I38346	elastin - hu
24	175	6.5	582	1 BNR73S	myelin-associated
25	175	6.5	626	1 BNR73S	myelin-associated
26	174	6.5	1091	2 A58532	glial cell membran
27	170.5	6.4	365	2 JC7780	coxsackie- and ade
28	170.5	6.4	3707	2 S18252	hepatan sulfate pr
29	164.5	6.1	847	2 JH0371	B-cell adhesion pr

30	162.5	6.1	278	1 TDRTOX	OX-2 membrane glyc
31	162.5	6.1	888	1 IURTNC	neutral cell adhesi
32	162	6.0	587	2 JH0464	DM-GRASP precursor
33	162	6.0	761	1 JH08NG	neutral cell adhesi
34	162	6.0	765	2 C42632	cell adhesion mole
35	162	6.0	812	2 B42632	cell adhesion mole
36	162	6.0	932	2 A42632	cell adhesion mole
37	161.5	6.0	739	2 JN0581	vascular cell adhe
38	160.5	6.0	702	2 A36319	carcinoembryonic a
39	160	6.0	725	2 IJMSNG	neutral cell adhesi
40	157	5.9	509	2 JC5288	SHP substrate-1 pr
41	157	5.9	1091	1 IJCHNL	SHP substrate-1 pr
42	156	5.8	646	2 I38049	neutral cell adhesi
43	155	5.8	513	2 JC5289	cell surface glyco
44	154	5.7	1612	2 T30805	SHP substrate-1 pr
45	153.5	5.7	1051	2 A39712	ductil protein - mo
					kinase-like protei

ALIGNMENTS

RESULT 1
T08732
hypothetical protein DKFZp566B0846.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C/Accession: T08732
R/Octenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, May 1999
A/Reference number: Z16474
A/Accession: T08732
A/Molecule type: mRNA
A/Residues: 1-407 <OTF>
A/Cross-references: EMBL:AL050071
A/Experimental source: fetal kidney; clone DKFZp566B0846
C/Genetics:
A/Note: DKFZp566B0846.1

Query Match 43.8%; Score 1173.5; DB 2; Length 407;
Best local similarity 62.8%; Pred. No. 4.5e-78;
Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7;

Qy	137	SGKYICKAVTPPLCNAQSSSTTVTVLEPVSILKGPDLIDGNETVAICIAATGKFA	196
Db	1	SGKYICKAVTPPLCNAQSSSTTVTVLEPVSILKGPDLIDGNETVAICIAATGKFA	60
Qy	197	HIDWEGDLMGESFTTSPNETATIIISQKLEPFRFARGRITCVKHPALKEKDIRYSFI	256
Db	61	HIDWEGDLMGESFTTSPNETATIIISQKLEPFRFARGRITCVKHPALKEKDIRYSFI	120
Qy	257	LDIQYAPRVSSTGIDGNMFGRKGNLKNADNPPPKSVMSRLDGMPPDGLASDNTL	316
Db	121	LDIQYAPRVSSTGIDGNMFGRKGNLKNADNPPPKSVMSRLDGMPPDGLASDNTL	180
Qy	317	HFVHPITRNSGVYICKVNTSLQSRSDQKVIYISDPV-----	353
Db	181	HFVHPITRNSGVYICKVNTSLQSRSDQKVIYISDPVTTTLPQTIOMHPSAIDEDLAT	240
Qy	354	-----FKQTSIAVAGVIGAVLALFIAIVTVLTPPRKK--RPSYLDKV	397
Db	241	EPKLPPLSLATIKDITATIIASVVGALFIVLSVAGIFCYRRRRTRRGYPPKN	300
Qy	398	IDLPPTH-----KPPLYEERSPPLPQKDLFQEHLL--PLQTFKREKRVG	440
Db	301	Y-IIPSDMQKESQIDVLQDDELDPYDGVKKNPNVNNIIRDYIESEPKTQW-----N	354
Qy	441	NLOHSGNLNRSFYEDENPVG	462
Db	355	NVENNMRP-ERPMDYEDLMKG	375

RESULT 2
JC4G24

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 15, 2002, 09:39:32 ; Search time 38 Seconds

(without alignments)
2976.839 Million cell updates/sec

Title: US-09-972-268-4

Sequence: 1 MATTGPSPSLCPGGKXQLS.....EDLVSHVDGVSISREMYV 549

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP rylus: *
16: SP bacteriophage: *
17: SP archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2887	99.4	549	4 Q9N0S3	Q9N0S3 homo sapien
2	2739	94.3	549	11 Q9U1B9	Q9U1B9 mus musculu
3	2695	92.8	549	11 Q9D006	Q9D006 mus musculu
4	2141	73.7	407	4 Q9Y412	Q9Y412 homo sapien
5	1832.5	62.1	510	11 Q9U1B8	Q9U1B8 mus musculu
6	1827.5	62.1	438	11 Q9U1B7	Q9U1B7 mus musculu
7	1629	56.1	304	4 Q9BVA9	Q9BVA9 homo sapien
8	544	18.7	510	4 Q96NY8	Q96NY8 homo sapien
9	543	18.7	510	4 Q96K15	Q96K15 homo sapien
10	542	18.7	101	4 Q8WVU4	Q8WVU4 homo sapien
11	534.5	18.4	295	11 Q9ERF5	Q9ERF5 mesocricetu
12	528	18.2	298	6 Q9GL74	Q9GL74 cercopithec
13	526.5	18.1	295	6 Q9GL75	Q9GL75 bos taurus
14	505	17.4	508	11 Q8R007	Q8R007 mus musculu
15	496	17.1	99	11 Q9CT80	Q9CT80 mus musculu
16	494	17.0	467	11 Q91VT9	Q91VT9 mus musculu

17	493.5	17.0	483	11 Q9NBP8	Q9NBP8 mus musculu
18	432	14.9	449	4 Q9UBT6	Q9UBT6 homo sapien
19	413.5	14.2	412	11 Q9B1E1	Q9B1E1 rattus norv
20	408.5	14.1	412	11 Q9B611	Q9B611 rattus norv
21	400.5	13.8	401	6 Q08835	Q08835 cercopithec
22	393	13.5	408	11 Q91WPI	Q91WPI mus musculu
23	390.5	13.4	417	4 Q96B31	Q96B31 homo sapien
24	346	11.9	415	11 Q60977	Q60977 mus musculu
25	337	11.6	494	11 Q9CR33	Q9CR33 mus musculu
26	336.5	11.6	456	11 Q8B5M8	Q8B5M8 mus musculu
27	334.5	11.5	442	4 Q9B577	Q9B577 homo sapien
28	334	11.5	445	11 Q9B411	Q9B411 mus musculu
29	271.5	9.3	336	11 Q9D6E7	Q9D6E7 mus musculu
30	250	8.6	261	11 Q9D6A9	Q9D6A9 mus musculu
31	247	8.5	396	11 Q9N288	Q9N288 mus musculu
32	234	8.1	959	5 Q9N9Y9	Q9N9Y9 drosophila
33	234	8.1	968	5 Q9M4T9	Q9M4T9 drosophila
34	233	8.0	306	11 Q9QYL4	Q9QYL4 mus musculu
35	233	8.0	432	4 Q9U0P1	Q9U0P1 homo sapien
36	229.5	7.9	975	5 Q97174	Q97174 drosophila
37	226.5	7.8	295	11 Q9QYL6	Q9QYL6 mus musculu
38	226.5	7.8	295	11 Q9Z2H8	Q9Z2H8 mus musculu
39	218	7.5	278	11 Q9QYL3	Q9QYL3 mus musculu
40	216	7.4	345	5 Q9M4U1	Q9M4U1 drosophila
41	215.5	7.4	4370	4 Q9H3V5	Q9H3V5 homo sapien
42	212.5	7.3	289	11 Q9QYL5	Q9QYL5 mus musculu
43	209	7.2	388	11 Q8R464	Q8R464 mus musculu
44	208	7.2	509	11 Q9QW15	Q9QW15 rattus norv
45	207	7.1	509	11 P97710	P97710 rattus norv

ALIGNMENTS

RESULT 1

Q9N0S3 ID Q9N0S3 PRELIMINARY; PRT; 549 AA.
AC Q9N0S3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Neectin 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Raymond N., Berg J.-P., Leccocq E., Adelaide J., Campadelli-Piune G.,
RT Dubreuil P., Lopez M.;
RT "Human neectin 3/PRK3: A novel member of the PVR/PRR/neectin family that
interacts with afadin.";
RL Gene 0:0-0(2000).
DR EMBL; AF282874; AAF97597.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR003600; IG like.
DR InterPro; IPR003606; IG like.
DR Pfam; PF00047; IG 2.
DR SMART; SM00409; IG 1.
DR SMART; SM00410; IG like; 1.
SQ SEQUENCE 549 AA; 61002 MW; 6D1104CBA9D731 CRC64;

Query Match 99.4%; Score 2887; DB 4; Length 549;
Best local similarity 99.4%; Pred. No. 1.2e-218;
Matches 547; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATTGPSPSLCPGGKXQLSASLIGALLPPPPPLILILPPLILFRLGALAGPI 60
DB 1 MATTGPSPSLCPGGKXQLSASLIGALLPPPPPLILILPPLILFRLGALAGPI 60
QY 61 IVEPHTAVMGKNSLSKCLIEVNEITTOISWEKHGKSSQTVAVHHPQYQFSYQYQGR 120
DB 61 IVEPHTAVMGKNSLSKCLIEVNEITTOISWEKHGKSSQTVAVHHPQYQFSYQYQGR 120

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QY 121 VLFRKYSNDATITLHNIGFSDSGKYCKAVTFPLGNAQSSSTTVTLVPTVSLIKGPD 180
DB 121 VLFRKYSNDATITLHNIGFSDSGKYCKAVTFPLGNAQSSSTTVTLVPTVSLIKGPD 180
QY 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFR 240
DB 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFR 240
QY 241 GRRITCVVKGHPALEKDIRYSFILDIOYAPEVSVTGIDGNMFVGRKGVNLKCNADANPPP 300
DB 241 GRRITCVVKGHPALEKDIRYSFILDIOYAPEVSVTGIDGNMFVGRKGVNLKCNADANPPP 300
QY 301 KSVMSRLDQWPGDGLASNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPT 360
DB 301 KSVMSRLDQWPGDGLASNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPT 360
QY 361 TTTLOPTIQWHPSTADIEDLATEPKLPPLSTLTIKDDTIATIIASVVGALFVLVS 420
DB 361 TTTLOPTIQWHPSTADIEDLATEPKLPPLSTLTIKDDTIATIIASVVGALFVLVS 420
QY 421 VLAGIFCYRRRTFRGDFYAKNYIPPSDMOKESQIDVLQDELDSDYPSVKKENKPNVN 480
DB 421 VLAGIFCYRRRTFRGDFYAKNYIPPSDMOKESQIDVLQDELDSDYPSVKKENKPNVN 480
QY 481 LIRKDYLEEPKQWNNVENLNRFERPMYDYLKMGKFPVSDHYDENEDDLVSHVDGS 540
DB 481 LIRKDYLEEPKQWNNVENLNRFERPMYDYLKMGKFPVSDHYDENEDDLVSHVDGS 540
QY 541 VISRREWTV 549
DB 541 VISRREWTV 549

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RESULT 2

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ID Q9JLB9 PRELIMINARY; PRT; 549 AA.
AC Q9JLB9;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Cell adhesion molecule nectin-3 alpha.
GN PVRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=1074716;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizouchi A., Takai Y.;
RT "Nectin-3, a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299 (2000).
DR EMBL; AF195833; AAF63685.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003600; IG_MHC.
DR Pfam; PF000047; ig_2.
DR SMART; SM00409; IG_1.
DR SMART; SM00410; IG_1like; 1.
SQ SEQUENCE 549 AA; 60583 MW; 5492C9ABB472F185 CRC64;

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Query Match 94.3%; Score 2739; DB 11; Length 549;
 Best Local Similarity 93.3%; Pred. No. 5.3e-207;
 Matches 512; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

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QY 1 MARYTGPSPICPGGGAQSSASLIGAGLILQPTTPPLLLILFLLPSRLCGALAGPI 60
DB 1 MARYTGPAPICPGGGAQSSAFFPAAGLLLPAPTTPPLLLILFLLPSRLCGALAGSI 60

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QY 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQVGFVSQGEYQGR 120
DB 61 IVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQVGFVSQGEYQGR 120
QY 121 VLFRKYSNDATITLHNIGFSDSGKYCKAVTFPLGNAQSSSTTVTLVPTVSLIKGPD 180
DB 121 VLFRKYSNDATITLHNIGFSDSGKYCKAVTFPLGNAQSSSTTVTLVPTVSLIKGPD 180
QY 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFR 240
DB 181 LIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFR 240
QY 241 GRRITCVVKGHPALEKDIRYSFILDIOYAPEVSVTGIDGNMFVGRKGVNLKCNADANPPP 300
DB 241 GRRITCVVKGHPALEKDIRYSFILDIOYAPEVSVTGIDGNMFVGRKGVNLKCNADANPPP 300
QY 301 KSVMSRLDQWPGDGLASNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPT 360
DB 301 KSVMSRLDQWPGDGLASNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPT 360
QY 361 TTTLOPTIQWHPSTADIEDLATEPKLPPLSTLTIKDDTIATIIASVVGALFVLVS 420
DB 361 TTTLOPTIQWHPSTADIEDLATEPKLPPLSTLTIKDDTIATIIASVVGALFVLVS 420
QY 421 VLAGIFCYRRRTFRGDFYAKNYIPPSDMOKESQIDVLQDELDSDYPSVKKENKPNVN 480
DB 421 VLAGIFCYRRRTFRGDFYAKNYIPPSDMOKESQIDVLQDELDSDYPSVKKENKPNVN 480
QY 481 LIRKDYLEEPKQWNNVENLNRFERPMYDYLKMGKFPVSDHYDENEDDLVSHVDGS 540
DB 481 LIRKDYLEEPKQWNNVENLNRFERPMYDYLKMGKFPVSDHYDENEDDLVSHVDGS 540
QY 541 VISRREWTV 549
DB 541 VISRREWTV 549

```

RESULT 3

```

ID Q9D006 PRELIMINARY; PRT; 549 AA.
AC Q9D006;
DT 01-JUN-2001 (TEMBLrel. 17, Created)
DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE 2610301B19RIK protein.
GN 2610301B19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=EMERYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateu Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Scorch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;

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